

SCORE Search Results Details for Application 10516759 and Search Result 20091123_110100_us-10-516-759a-14_copy_24_81.rag.

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This page gives you Search Results detail for the Application 10516759 and Search Result 20091123_110100_us-10-516-759a-14_copy_24_81.rag.

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OM protein - protein search, using sw model

Run on: November 23, 2009, 11:13:51 ; Search time 57 Seconds
(without alignments)
960.024 Million cell updates/sec

Title: US-10-516-759A-14_COPY_24_81
Perfect score: 350
Sequence: 1 DIKHNRPRRDCVAEGKVCDP.....RNYSRGGVCVTHCNFLNGEP 58

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5029790 seqs, 943472257 residues

Total number of hits satisfying chosen parameters: 5029790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200907:*
1: geneseqp1:*
2: geneseqp2:*
3: geneseqp3:*

SUMMARIES

Result		Query					
No.	Score	Match	Length	DB	ID	Description	

1	350	100.0	82	1	ADE36725	Ade36725	Human	Erb
2	350	100.0	89	1	ADE36731	Ade36731	Human	Erb
3	350	100.0	531	2	AJE77228	Aje77228	Human	Erb
4	350	100.0	569	2	AOJ20844	Aoj20844	Human	Erb
5	350	100.0	569	3	AUP69764	Aup69764	Human	Erb
6	350	100.0	570	2	AEH24404	Aeh24404	HUMEGFRBB	
7	350	100.0	621	2	AOG42613	Aog42613	Human	HER
8	350	100.0	621	2	AOG42228	Aog42228	Human	HER
9	350	100.0	624	2	AEH24397	Aeh24397	HUMEGFRBB	
10	350	100.0	624	2	AEH24406	Aeh24406	HUMEGFRBB	
11	350	100.0	625	2	ATT39332	Att39332	Human	ERB
12	350	100.0	626	2	ATT39333	Att39333	Human	ERB
13	350	100.0	640	1	ADE36713	Ade36713	Human	Erb
14	350	100.0	640	1	ADW39268	Adw39268	Human	Erb
15	350	100.0	699	2	AEH24399	Aeh24399	HUMEGFRBB	
16	350	100.0	824	2	ATT39331	Att39331	Human	ERB
17	350	100.0	843	2	ATT39330	Att39330	Human	ERB
18	350	100.0	857	2	AOG42248	Aog42248	Human	HER
19	350	100.0	866	2	AOG42602	Aog42602	Human	HER
20	350	100.0	1298	2	AEK41239	Aek41239	Human	tyr
21	350	100.0	1300	2	AOJ20843	Aoj20843	Human	Erb
22	350	100.0	1302	2	AOJ20845	Aoj20845	Human	Erb
23	350	100.0	1342	1	AAR13833	Aar13833	HER-3	epi
24	350	100.0	1342	1	AAR88453	Aar88453	erbB-3	po
25	350	100.0	1342	1	AAW69406	Aaw69406	ErbB-3	gl
26	350	100.0	1342	1	AAAY16594	Aay16594	erbB-3	pr
27	350	100.0	1342	1	AAG65359	Aag65359	Human	Her
28	350	100.0	1342	1	ADE62708	Ade62708	Human	Pro
29	350	100.0	1342	1	ADB67646	Adb67646	Human	epi
30	350	100.0	1342	1	ADB67617	Adb67617	Human	epi
31	350	100.0	1342	1	ADB67645	Adb67645	Human	epi
32	350	100.0	1342	1	ADB67647	Adb67647	Human	epi
33	350	100.0	1342	1	ADB67642	Adb67642	Human	epi
34	350	100.0	1342	1	ADB67644	Adb67644	Human	epi
35	350	100.0	1342	1	ADB67643	Adb67643	Human	epi
36	350	100.0	1342	1	ADN39920	Adn39920	Cancer/an	
37	350	100.0	1342	1	ADA37256	Ada37256	Human	Erb
38	350	100.0	1342	1	ADM10301	Adm10301	Human	epi
39	350	100.0	1342	1	ADD52685	Add52685	Human	erb
40	350	100.0	1342	1	ADE36712	Ade36712	Human	Erb
41	350	100.0	1342	1	ADW39267	Adw39267	Human	Erb
42	350	100.0	1342	1	ADJ66656	Adj66656	Her3	prot
43	350	100.0	1342	1	ADO56208	Ado56208	Human	Erb
44	350	100.0	1342	1	ADP54346	Adp54346	Human	PRO
45	350	100.0	1342	1	ADQ19366	Adq19366	Human	sof

ALIGNMENTS

RESULT 1

ADE36725

ID ADE36725 standard; protein; 82 AA.

XX

AC ADE36725;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human ErbB-3-f12 amino acid sequence SEQ ID NO:14.

XX

KW neoplasm; ErbB-3; immune response; cytostatic; gene therapy; cancer;
KW human.

XX

OS Homo sapiens.

XX

PN WO2003080835-A1.

XX

PD 02-OCT-2003.

XX

PF 26-MAR-2003; 2003WO-CN000217.

XX

PR 26-MAR-2002; 2002CN-00116259.

XX

PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.

XX

PI Zhou M;

XX

DR WPI; 2003-876924/81.

XX

PT Use of an ErbB-3 protein, a nucleic acid encoding an ErbB-3 protein or
PT their fragments, for treating, preventing or delaying neoplasms (e.g.
PT urethra, uterus, vagina or vulva neoplasm) or cancers (e.g. breast, ovary
PT or colon cancer).

XX

PS Claim 22; SEQ ID NO 14; 68pp; English.

XX

CC The present invention describes a method for treating, preventing or
CC delaying neoplasm in a mammal. The method comprises administering an ErbB
CC -3 protein, a nucleic acid encoding an ErbB-3 protein, or their
CC functional fragments, where an immune response is generated against the
CC neoplasm. ErbB-3 has cytostatic activity, and can be used in gene
CC therapy. The method is useful for treating, preventing or delaying
CC neoplasms (e.g. adrenal gland, anus, auditory nerve, bile ducts, bladder,
CC bone, brain, breast, buccal, central nervous system, cervix, colon, ear,
CC endometrium, oesophagus, eye, eyelids, fallopian tube, gastrointestinal
CC tract, head and neck, heart, kidney, larynx, liver, lung, mandible,
CC mandibular condyle, maxilla, mouth, nasopharynx, nose, oral cavity,

CC ovary, pancreas, parotid gland, penis, pinna, pituitary, prostate gland,
CC rectum, retina, salivary glands, skin, small intestine, spinal cord,
CC stomach, testes, thyroid, tonsil, urethra, uterus, vagina,
CC vestibulocochlear nerve, or vulva neoplasm), or cancers (breast, ovary,
CC stomach, prostate, colon and lung cancer). The present sequence
CC represents a human ErbB-3 amino acid sequence, which is used in the
CC exemplification of the present invention. N.B. The present sequence is
CC designated as SEQ ID NO:14 in the Sequence Listing but does not
CC correspond with the SEQ ID NO:14 given in figure 23.
XX
SQ Sequence 82 AA;

Query Match 100.0%; Score 350; DB 1; Length 82;
Best Local Similarity 100.0%;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 24 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 81

RESULT 2
ADE36731

ID ADE36731 standard; protein; 89 AA.
XX
AC ADE36731;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human ErbB-3-f12 amino acid sequence SEQ ID NO:14.
XX
KW neoplasm; ErbB-3; immune response; cytostatic; gene therapy; cancer;
KW human.
XX
OS Homo sapiens.
XX
PN WO2003080835-A1.
XX
PD 02-OCT-2003.
XX
PF 26-MAR-2003; 2003WO-CN000217.
XX
PR 26-MAR-2002; 2002CN-00116259.
XX
PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.
XX
PI Zhou M;
XX
DR WPI; 2003-876924/81.

http://es/ScoreAccessWeb/GetItem.action?AppId=105167...10-516-759a-14_copy_24_81.rag&ItemType=4&startByte=0 (5 of 25)11/30/2009 3:01:17 PM

DE Human ErbB3 tyrosine kinase receptor ectodomain protein (aa: 1-531).
 XX
 KW Diagnosis; prognosis; therapeutic; cancer;
 KW ErbB3 tyrosine kinase receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2007092932-A2.
 XX
 PD 16-AUG-2007.
 XX
 PF 08-FEB-2007; 2007WO-US061863.
 XX
 PR 08-FEB-2006; 2006US-0771237P.
 PR 05-OCT-2006; 2006US-0828343P.
 XX
 PA (TARG-) TARGETED MOLECULAR DIAGNOSTICS LLC.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bacus SS, Hill JE, Yarden Y, Kochupurakkal BS;
 XX
 DR WPI; 2007-690352/64.
 DR N-PSDB; AJE77227.
 DR REFSEQ; NP_001973.
 XX
 PT New bivalent binding molecule having binding affinity for ErbB ligand at
 PT separate binding sites in a single covalently joined protein molecule,
 PT useful for treating a disease or condition by removal or inhibition of an
 PT ErbB ligand.
 XX
 PS Claim 10; SEQ ID NO 6; 37pp; English.
 XX
 CC The present invention relates to new bivalent ErbB-based ligand binding
 CC molecules along with their method of preparation and use. The binding
 CC molecule can be a protein expressed from a recombinant DNA molecule and
 CC contain two extracellular domains of an ErbB receptor wherein both the
 CC domains bind to ErbB receptor ligands. These binding molecules act as
 CC traps to bind and sequester ligands, thus making them unavailable for
 CC binding to cellular ErbB receptors. The bivalent binding molecules and
 CC methods of the invention are useful for diagnosing and prognosing cancer
 CC and treating a disease or condition that is improved, ameliorated or
 CC inhibited by removal or inhibition of an ErbB ligand. The present
 CC sequence is human erythroblastic leukemia viral oncogene homolog 3
 CC tyrosine kinase receptor (ErbB3 tyrosine kinase receptor; HER3) receptor
 CC ectodomain protein. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 531 AA;

Query Match 100.0%; Score 350; DB 2; Length 531;
 Best Local Similarity 100.0%;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 464 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 521

RESULT 4

AOJ20844

ID AOJ20844 standard; protein; 569 AA.

XX

AC AOJ20844;

XX

DT 06-MAR-2008 (first entry)

XX

DE Human ErbB3 receptor tyrosine kinase protein SEQ:97.

XX

KW splicing; gene identification signature analysis; therapeutic; diagnosis;

KW cancer; cytostatic; inflammation; antiinflammatory; autoimmune disease;

KW immunosuppressive; graft rejection.

XX

OS Homo sapiens.

XX

PN WO2005071059-A2.

XX

PD 04-AUG-2005.

XX

PF 27-JAN-2005; 2005WO-IL000107.

XX

PR 27-JAN-2004; 2004US-0539128P.

PR 15-JUN-2004; 2004US-0579202P.

XX

PA (COMP-) COMPUGEN LTD.

XX

PI Sorek R, Pollock S, Diber A, Levine Z, Nemzer S, Kol G, Wool A;

PI Haviv A, Cohen Y, Cohen Y, Shemesh R, Savitsky K;

XX

DR WPI; 2005-555488/56.

XX

PT Identifying alternatively spliced exons, involves scoring each of several

PT exon sequences derived from genes of species according to one or more

PT sequence parameters.

XX

PS Example 3; SEQ ID NO 97; 991pp; English.

XX

CC The present invention relates to a novel method of identifying (M1)

alternatively spliced exons. The method comprises scoring each of several exon sequences derived from genes of a species according to at least one sequence parameter, where the exon sequences of the several exon sequences scoring above a predetermined threshold represent alternatively spliced exons, thus identifying the alternatively spliced exons. Also claimed are: a system (S1) for generating a database of alternatively spliced exons; predicting (M2) expression products of a gene of interest and analyzing chromosomal location of each of the alternatively spliced exons with respect to coding sequence of the gene of interest to thus predict expression products of the gene of interest. (M1) is useful for identifying alternatively spliced exons. (S1) is useful for generating a database of alternatively spliced exons. The DNA and the protein sequences of the invention are useful for the diagnosis and/or treatment of the diseases like cancer, inflammatory disease, autoimmune disease, allergy and graft rejection. The present sequence represents a human ErbB3 receptor tyrosine kinase protein.

Sequence 569 AA;

```
Query Match      100.0%;   Score 350;   DB 2;   Length 569;
Best Local Similarity 100.0%;
Matches    58;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
```

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 ||||||||||||||||||
 Db 483 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

RESULT 5

AUP69764

ID AUP69764 standard; protein; 569 AA.

XX

AC AUP69764;

XX

DT 19-FEB-2009 (first entry)

XX

DE Human Erbb3 tyrosine kinase receptor (delta15HER3) protein SEQ ID NO: 12.

XX

KW tumor marker; protein therapy; therapeutic; ovary tumor; cytostatic;
KW endocrine-gen.; gynecological; uropathic; breast tumor;
KW hyperproliferation; cancer; lung tumor; respiratory-gen.; stomach tumor;
KW gastrointestinal-gen.; colon tumor; pulmonary fibrosis; antiinflammatory;
KW Erbb3 tyrosine kinase receptor; HER3;
KW human epidermal growth factor receptor 3.

XX

OS Homo sapiens.

XX

PN WO2008153933-A2.

XX


```
Query Match      100.0%;   Score 350;   DB 3;   Length 569;
Best Local Similarity 100.0%;
Matches    58;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
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http://es/ScoreAccessWeb/GetItem.action?AppId=105167...10-516-759a-14_copy_24_81.rag&ItemType=4&startByte=0 (9 of 25)11/30/2009 3:01:17 PM

Db 483 DIKHNRPRRDCVAEGKVCDP LCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

RESULT 6

AEH24404

ID AEH24404 standard; protein; 570 AA.

XX

AC AEH24404;

XX

DT 29-JUN-2006 (first entry)

XX

DE HUMEGFRBB3_PEA_1_P53 polypeptide.

XX

KW diagnostic; prognosis; genetic marker; screening; cancer; cytostatic;
 KW neoplasm; HUMEGFRBB3_PEA_1_P53; protein-tyrosine kinase erbB-3 precursor;
 KW ERBB3.

XX

OS Homo sapiens.

XX

PN WO2006043271-A1.

XX

PD 27-APR-2006.

XX

PF 16-OCT-2005; 2005WO-IL001096.

XX

PR 22-OCT-2004; 2004US-0621004P.

PR 18-NOV-2004; 2004US-0628529P.

XX

PA (COMP-) COMPUGEN LTD.

XX

PI Novik A, Pollock S, Levine Z, Dahary D, Sorek R, Sella-Tavor O;
 PI Cohen-Dayag A, Sameach-Greenwald S, Walach S;

XX

DR WPI; 2006-331789/34.

DR N-PSDB; AEH24321.

XX

PT New isolated polynucleotide and polypeptide markers, useful as diagnostic
 PT markers for diagnosing diseases, predicting response to treatment,
 PT monitoring treatment, or determining prognosis of a marker-detectable
 PT disease.

XX

PS Example 5; SEQ ID NO 144; 421pp; English.

XX

CC The invention describes an isolated polynucleotide comprising
 CC HUMA1ACM_PEA 2 _T21, HUMA1ACM_PEA 2 _T27, or HUMA1ACM_PEA 2 _T7
 CC comprising 1320, 1239, or 2713 bp (SEQ ID NO. 1, 2, or 3). Also described
 CC are: an isolated polypeptide selected from HUMA1ACM_PEA 2 _P36 (SEQ ID
 CC NO. 51), HUMA1ACM_PEA 2 _P49 (SEQ ID NO. 52), or HUMA1ACM_PEA 2 _P59 (SEQ
 CC ID NO. 53); an isolated polypeptide encoding for a head of: (a)

CC HUMA1ACM_PEA 2 _P36 comprising a polypeptide 70% homologous to SEQ ID NO.
 CC 180 or 182 of HUMA1ACM_PEA 2 _P36; (b) HUMA1ACM_PEA 2 _P49 comprising a
 CC polypeptide 70% homologous to SEQ ID NO. 182 of HUMA1ACM_PEA 2 _P49; or
 CC (c) HUMA1ACM_PEA 2 _P59 comprising a polypeptide 70% homologous to SEQ ID
 CC NO. 182 of HUMA1ACM_PEA 2 _P59; an isolated polypeptide encoding for a
 CC tail of: (a) HUMA1ACM_PEA 2 _P36 comprising a polypeptide 70% homologous
 CC to SEQ ID NO. 181 in HUMA1ACM_PEA 2 _P36; (b) HUMA1ACM_PEA 2 _P49
 CC comprising a polypeptide 70% homologous to SEQ ID NO. 183 in HUMA1ACM_PEA
 CC 2 _P49; or (c) HUMA1ACM_PEA 2 _P59 comprising a polypeptide 70%
 CC homologous to SEQ ID NO. 185 or 208 in HUMA1ACM_PEA 2 _P59; a primer pair
 CC comprising a pair of isolated oligonucleotides capable of amplifying the
 CC amplicon; an antibody capable of specifically binding to an epitope of
 CC the amino acid sequence; a kit for detecting a marker-detectable disease
 CC comprising a kit detecting specific expression of a splice variant; a
 CC biomarker capable of detecting marker-detectable disease comprising the
 CC nucleic acid sequences or amino acid sequence, or its fragments. The
 CC polynucleotides and polypeptides are useful as diagnostic markers for
 CC diagnosing and screening for diseases diseases e.g., cancer, selecting a
 CC therapy for a marker-detectable disease and determining prognosis of a
 CC marker-detectable disease, as well as for predicting response to
 CC treatment and monitoring treatment. This sequence represents a
 CC HUMEGRFRBB3_PEA_1_P53 polypeptide, a transcript from the HUMEGRFRBB3
 CC cluster and variant of protein-tyrosine kinase erbB-3 precursor useful as
 CC a diagnostic marker.
 XX
 SQ Sequence 570 AA;

Query Match 100.0%; Score 350; DB 2; Length 570;
 Best Local Similarity 100.0%;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCVAEGKVCPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||
 Db 483 DIKHNRPRRDCVAEGKVCPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

RESULT 7
 AOG42613
 ID AOG42613 standard; protein; 621 AA.
 XX
 AC AOG42613;
 XX
 DT 06-MAR-2008 (first entry)
 XX
 DE Human HER3 receptor extracellular domain (HF310) mutant protein.
 XX
 KW Therapeutic; cancer; cytostatic; pancreas tumor; stomach tumor;
 KW head & neck tumor; uterine cervix tumor; lung tumor; colorectal tumor;
 KW endometroid carcinoma; prostate tumor; esophagus tumor; ovary tumor;

KW uterus tumor; glioma; bladder tumor; renal tumor; breast tumor;
 KW hyperproliferation; ocular disease; ophthalmological;
 KW diabetic retinopathy; antidiabetic; psoriasis; antipsoriatic; restenosis;
 KW vasotropic; stenosis; atherosclerosis; antiarteriosclerotic;
 KW chronic obstructive airway disease; respiratory-gen.; inflammation;
 KW antiinflammatory; angiogenesis disorder; antiangiogenic; gene therapy;
 KW HER3; receptor; ErbB3; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 541

FT /note= "Wild type Gly replaced with Glu"

XX

PN WO2007146959-A2.

XX

PD 21-DEC-2007.

XX

PF 12-JUN-2007; 2007WO-US071041.

XX

PR 12-JUN-2006; 2006US-0813260P.

PR 29-SEP-2006; 2006US-0848542P.

PR 05-JAN-2007; 2007US-0878941P.

XX

PA (RECE-) RECEPTOR BIOLOGIX INC.

XX

PI Shepard HM, Jin P, Burton LE, Beryt M;

XX

DR WPI; 2008-B51284/10.

XX

PT New multimer comprising extracellular domain ECD from HER1 receptor,
 PT useful for treating cancer, inflammatory disease, angiogenic disease or
 PT hyperproliferative disease.

XX

PS Disclosure; Page; 320pp; English.

XX

CC The present invention provides pan-cell surface receptor specific
 CC therapeutics including and pan-HER (also referred to as ErbB or EGFR)
 CC specific therapeutics that interact with at least two different HER
 CC receptor ligands and/or dimerize with or interact with two or more HER
 CC cell surface receptors. The invention is useful for treating cancer such
 CC as pancreatic, gastric, head and neck, cervical, lung, colorectal,
 CC endometrial, prostate, esophageal, ovarian, uterine, glioma, bladder,
 CC renal and breast cancer, proliferative diseases such as proliferation
 CC and/or migration of smooth muscle cells, disease of the anterior eye,
 CC diabetic retinopathy, psoriasis, restenosis, ophthalmic disorders,
 CC stenosis, atherosclerosis, hypertension from thickening of blood vessels,
 CC bladder diseases and obstructive airway diseases, inflammatory disease

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||
 Db 464 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 521

AC AEH24397;
 XX
 DT 29-JUN-2006 (first entry)
 XX
 DE HUMEGFRBB3_PEA_1_P15 polypeptide.
 XX
 KW diagnostic; prognosis; genetic marker; screening; cancer; cytostatic;
 KW neoplasm; HUMEGFRBB3_PEA_1_P15; protein-tyrosine kinase erbB-3 precursor;
 KW ERBB3.
 XX
 OS Homo sapiens.
 XX
 PN WO2006043271-A1.
 XX
 PD 27-APR-2006.
 XX
 PF 16-OCT-2005; 2005WO-IL001096.
 XX
 PR 22-OCT-2004; 2004US-0621004P.
 PR 18-NOV-2004; 2004US-0628529P.
 XX
 PA (COMP-) COMPUGEN LTD.
 XX
 PI Novik A, Pollock S, Levine Z, Dahary D, Sorek R, Sella-Tavor O;
 PI Cohen-Dayag A, Sameach-Greenwald S, Walach S;
 XX
 DR WPI; 2006-331789/34.
 DR N-PSDB; AEH24320.
 XX
 PT New isolated polynucleotide and polypeptide markers, useful as diagnostic
 PT markers for diagnosing diseases, predicting response to treatment,
 PT monitoring treatment, or determining prognosis of a marker-detectable
 PT disease.
 XX
 PS Example 5; SEQ ID NO 137; 421pp; English.
 XX
 CC The invention describes an isolated polynucleotide comprising
 CC HUMA1ACM_PEA 2 _T21, HUMA1ACM_PEA 2 _T27, or HUMA1ACM_PEA 2 _T7
 CC comprising 1320, 1239, or 2713 bp (SEQ ID NO. 1, 2, or 3). Also described
 CC are: an isolated polypeptide selected from HUMA1ACM_PEA 2 _P36 (SEQ ID
 CC NO. 51), HUMA1ACM_PEA 2 _P49 (SEQ ID NO. 52), or HUMA1ACM_PEA 2 _P59 (SEQ
 CC ID NO. 53); an isolated polypeptide encoding for a head of: (a)
 CC HUMA1ACM_PEA 2 _P36 comprising a polypeptide 70% homologous to SEQ ID NO.
 CC 180 or 182 of HUMA1ACM_PEA 2 _P36; (b) HUMA1ACM_PEA 2 _P49 comprising a
 CC polypeptide 70% homologous to SEQ ID NO. 182 of HUMA1ACM_PEA 2 _P49; or
 CC (c) HUMA1ACM_PEA 2 _P59 comprising a polypeptide 70% homologous to SEQ ID
 CC NO. 182 of HUMA1ACM_PEA 2 _P59; an isolated polypeptide encoding for a
 CC tail of: (a) HUMA1ACM_PEA 2 _P36 comprising a polypeptide 70% homologous
 CC to SEQ ID NO. 181 in HUMA1ACM_PEA 2 _P36; (b) HUMA1ACM_PEA 2 _P49

```
Query Match      100.0%;   Score 350;   DB 2;   Length 624;
Best Local Similarity 100.0%;
Matches    58;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
```

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||||||||||||||||||||
 Db 483 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

AEH24406

ID AEH24406 standard; protein; 624 AA.

XX

AC AEH24406;

XX

DT 29-JUN-2006 (first entry)

XX

DE HUMEGFRBB3_PEA_1_P55 polypeptide.

XX

KW diagnostic; prognosis; genetic marker; screening; cancer; cytostatic;
KW neoplasm; HMEGFRBB3_PEA_1_P55; protein-tyrosine kinase erbB-3 precursor;
KW ERBB3.

XX

OS Homo sapiens.

XX

PN WO2006043271-A1.

XX

PD 27-APR-2006.

XX

PF 16-OCT-2005; 2005WO-IL001096.

XX

PR 22-OCT-2004; 2004US-0621004P.

PR 18-NOV-2004; 2004US-0628529P.

XX

PA (COMP-) COMPUGEN LTD.

XX

PI Novik A, Pollock S, Levine Z, Dahary D, Sorek R, Sella-Tavor O;

PI Cohen-Dayag A, Sameach-Greenwald S, Walach S;

XX

DR WPI; 2006-331789/34.

DR N-PSDB; AEH24323.

XX

PT New isolated polynucleotide and polypeptide markers, useful as diagnostic
PT markers for diagnosing diseases, predicting response to treatment,
PT monitoring treatment, or determining prognosis of a marker-detectable
PT disease.

XX

PS Example 5; SEQ ID NO 146; 421pp; English.

XX

CC The invention describes an isolated polynucleotide comprising
CC HUMA1ACM_PEA 2 _T21, HUMA1ACM_PEA 2 _T27, or HUMA1ACM_PEA 2 _T7
CC comprising 1320, 1239, or 2713 bp (SEQ ID NO. 1, 2, or 3). Also described
CC are: an isolated polypeptide selected from HUMA1ACM_PEA 2 _P36 (SEQ ID
CC NO. 51), HUMA1ACM_PEA 2 _P49 (SEQ ID NO. 52), or HUMA1ACM_PEA 2 _P59 (SEQ
CC ID NO. 53); an isolated polypeptide encoding for a head of: (a)
CC HUMA1ACM_PEA 2 _P36 comprising a polypeptide 70% homologous to SEQ ID NO.
CC 180 or 182 of HUMA1ACM_PEA 2 _P36; (b) HUMA1ACM_PEA 2 _P49 comprising a
CC polypeptide 70% homologous to SEQ ID NO. 182 of HUMA1ACM_PEA 2 _P49; or
CC (c) HUMA1ACM_PEA 2 _P59 comprising a polypeptide 70% homologous to SEQ ID
CC NO. 182 of HUMA1ACM_PEA 2 _P59; an isolated polypeptide encoding for a
CC tail of: (a) HUMA1ACM_PEA 2 _P36 comprising a polypeptide 70% homologous
CC to SEQ ID NO. 181 in HUMA1ACM_PEA 2 _P36; (b) HUMA1ACM_PEA 2 _P49
CC comprising a polypeptide 70% homologous to SEQ ID NO. 183 in HUMA1ACM_PEA
CC 2 _P49; or (c) HUMA1ACM_PEA 2 _P59 comprising a polypeptide 70%
CC homologous to SEQ ID NO. 185 or 208 in HUMA1ACM_PEA 2 _P59; a primer pair
CC comprising a pair of isolated oligonucleotides capable of amplifying the
CC amplicon; an antibody capable of specifically binding to an epitope of
CC the amino acid sequence; a kit for detecting a marker-detectable disease
CC comprising a kit detecting specific expression of a splice variant; a
CC biomarker capable of detecting marker-detectable disease comprising the
CC nucleic acid sequences or amino acid sequence, or its fragments. The
CC polynucleotides and polypeptides are useful as diagnostic markers for
CC diagnosing and screening for diseases diseases e.g., cancer, selecting a
CC therapy for a marker-detectable disease and determining prognosis of a
CC marker-detectable disease, as well as for predicting response to
CC treatment and monitoring treatment. This sequence represents a
CC HUMEGFRBB3_PEA_1_P55 polypeptide, a transcript from the HUMEGFRBB3
CC cluster and variant of protein-tyrosine kinase erbB-3 precursor useful as

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Query Match      100.0%;   Score 350;   DB 2;   Length 624;
Best Local Similarity 100.0%;
Matches    58;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
```

Qy 1 DIKHNRRPRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||
 Db 483 DIKHNRRPRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

ATT39332

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XX

OS Synthetic.

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XX

XX

XX

XX

DR WPI; 2008-015609/82.

XX

PT New compound that comprises an independently folding protein domain fused

PT to a second independently folding protein domain by non-peptide bond for

PT treating e.g. cancer, metastatic disease, asthma, rheumatoid arthritis

PT and autoimmune disease.

XX

PS Example 9; SEQ ID NO 193; 363pp; English.

XX

CC The present invention relates to a novel compound comprising an

CC independently folding protein domain fused to a second independently

CC folding protein domain by a non-peptide bond around which dihedral

CC rotation may occur. The invention, in particular, relates to hybrid

CC immunoglobulins containing moving parts, related compositions, methods of

CC use, methods of production of such hybrid immunoglobulins; and to

CC analogous genetic devices, preferably nanodevices. The protein-like

CC compounds (preferably immunoglobulins) and their dimers and multimers are

CC useful for affecting the activity of a target, e.g. epidermal growth

CC factor (EGF) receptor, human epidermal growth factor receptor 2 (HER2),

CC vascular endothelial growth factor (VEGF) receptor (e.g. VEGFR1, VEGFR6,

CC and VEGFR3), CD20 antigen, CD11a leukocyte receptor, IgE immunoglobulin,

CC glycoprotein IIa receptor, glycoprotein IIIa receptor, tumor necrosis

CC factor (TNF) alpha (e.g. TNFRSF1a, and TNFRSF1b), or TNF receptor, gap

CC protein 120 (gp120), human Erbb1 (proto-oncogene), Erb2, Erb6, Erb3 and

CC Erb4; useful for treating e.g. cancer, metastatic disease, B-cell non-

CC Hodgkin's lymphoma, asthma, a subject having a skin test positive for

CC perennial aerocollagen, rheumatoid arthritis, psoriatic arthritis,

CC ankylosing spondylitis, Crohn's disease, fistulizing disease, metastatic

CC colorectal carcinoma, as an adjunct to percutaneous coronary

CC intervention, and autoimmune diseases. The present sequence represents a

CC fusion protein comprising the human Erbb3 tyrosine kinase receptor fused

CC with the human intein polypeptide which was useful during the method of

CC the invention for the production of hybrid immunoglobulins.

XX

SQ Sequence 625 AA;

Query Match 100.0%; Score 350; DB 2; Length 625;

Best Local Similarity 100.0%;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58

Db 464 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 521

RESULT 12

ATT39333

ID ATT39333 standard; protein; 626 AA.

XX

AC ATT39333;

XX
DT 08-JAN-2009 (first entry)
XX
DE Human ERBB3-intein fusion protein SEQ ID 194.
XX
KW protein production; chimeric protein; nanotechnology;
KW antibody engineering; antibody production; gene regulation;
KW antibody therapy; therapeutic; cancer; metastasis; non-hodgkin lymphoma;
KW asthma; rheumatoid arthritis; psoriatic arthritis;
KW ankylosing spondylitis; Crohns disease; colorectal tumor;
KW autoimmune disease; antiallergic; antiarthritic; antiasthmatic;
KW antiinflammatory; cytostatic; gastrointestinal-gen.; hematological-gen.;
KW immunomodulator; immunosuppressive; musculoskeletal-gen.;
KW respiratory-gen.; Erbb3 tyrosine kinase receptor; intein; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2008254512-A1.
XX
PD 16-OCT-2008.
XX
PF 31-OCT-2007; 2007US-00982085.
XX
PR 02-NOV-2006; 2006US-0856864P.
XX
PA (CAPO/) CAPON D J.
XX
PI Capon DJ;
XX
DR WPI; 2008-015609/82.
XX
PT New compound that comprises an independently folding protein domain fused
PT to a second independently folding protein domain by non-peptide bond for
PT treating e.g. cancer, metastatic disease, asthma, rheumatoid arthritis
PT and autoimmune disease.
XX
PS Example 9; SEQ ID NO 194; 363pp; English.
XX
CC The present invention relates to a novel compound comprising an
CC independently folding protein domain fused to a second independently
CC folding protein domain by a non-peptide bond around which dihedral
CC rotation may occur. The invention, in particular, relates to hybrid
CC immunoglobulins containing moving parts, related compositions, methods of
CC use, methods of production of such hybrid immunoglobulins; and to
CC analogous genetic devices, preferably nanodevices. The protein-like
CC compounds (preferably immunoglobulins) and their dimers and multimers are
CC useful for affecting the activity of a target, e.g. epidermal growth
CC factor (EGF) receptor, human epidermal growth factor receptor 2 (HER2),

CC vascular endothelial growth factor (VEGF) receptor (e.g. VEGFR1, VEGFR6,
CC and VEGFR3), CD20 antigen, CD11a leukocyte receptor, IgE immunoglobulin,
CC glycoprotein IIa receptor, glycoprotein IIIa receptor, tumor necrosis
CC factor (TNF) alpha (e.g. TNFRSF1a, and TNFRSF1b), or TNF receptor, gap
CC protein 120 (gp120), human Erbb1 (proto-oncogene), Erb2, Erb6, Erb3 and
CC Erb4; useful for treating e.g. cancer, metastatic disease, B-cell non-
CC Hodgkin's lymphoma, asthma, a subject having a skin test positive for
CC perennial aerocollagen, rheumatoid arthritis, psoriatic arthritis,
CC ankylosing spondylitis, Crohn's disease, fustulizing disease, metastatic
CC colorectal carcinoma, as an adjunct to percutaneous coronary
CC intervention, and autoimmune diseases. The present sequence represents a
CC fusion protein comprising the human Erbb3 tyrosine kinase receptor fused
CC with the human intein polypeptide which was useful during the method of
CC the invention for the production of hybrid immunoglobulins.
XX
SQ Sequence 626 AA;

Query Match 100.0%; Score 350; DB 2; Length 626;
Best Local Similarity 100.0%;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||||
Db 464 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 521

RESULT 13
ADE36713
ID ADE36713 standard; protein; 640 AA.
XX
AC ADE36713;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human ErbB-3 partial amino acid sequence SEQ ID NO:2.
XX
KW neoplasm; ErbB-3; immune response; cytostatic; gene therapy; cancer;
KW human.
XX
OS Homo sapiens.
XX
PN WO2003080835-A1.
XX
PD 02-OCT-2003.
XX
PF 26-MAR-2003; 2003WO-CN000217.
XX
PR 26-MAR-2002; 2002CN-00116259.
XX


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Query Match      100.0%;   Score 350;   DB 1;   Length 640;
Best Local Similarity 100.0%;
Matches    58;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
```

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||
 Db 483 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

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RESULT 15
AEH24399
ID      AEH24399 standard; protein; 699 AA.
XX
AC      AEH24399;
XX

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DT 29-JUN-2006 (first entry)
XX
DE HUMEGFRBB3_PEA_1_P31 polypeptide.
XX
KW diagnostic; prognosis; genetic marker; screening; cancer; cytostatic;
KW neoplasm; HUMEGFRBB3_PEA_1_P31; protein-tyrosine kinase erbB-3 precursor;
KW ERBB3.
XX
OS Homo sapiens.
XX
PN WO2006043271-A1.
XX
PD 27-APR-2006.
XX
PF 16-OCT-2005; 2005WO-IL001096.
XX
PR 22-OCT-2004; 2004US-0621004P.
PR 18-NOV-2004; 2004US-0628529P.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Novik A, Pollock S, Levine Z, Dahary D, Sorek R, Sella-Tavor O;
PI Cohen-Dayag A, Sameach-Greenwald S, Walach S;
XX
DR WPI; 2006-331789/34.
DR N-PSDB; AEH24326.
XX
PT New isolated polynucleotide and polypeptide markers, useful as diagnostic
PT markers for diagnosing diseases, predicting response to treatment,
PT monitoring treatment, or determining prognosis of a marker-detectable
PT disease.
XX
PS Example 5; SEQ ID NO 139; 421pp; English.
XX
CC The invention describes an isolated polynucleotide comprising
CC HUMA1ACM_PEA 2 _T21, HUMA1ACM_PEA 2 _T27, or HUMA1ACM_PEA 2 _T7
CC comprising 1320, 1239, or 2713 bp (SEQ ID NO. 1, 2, or 3). Also described
CC are: an isolated polypeptide selected from HUMA1ACM_PEA 2 _P36 (SEQ ID
CC NO. 51), HUMA1ACM_PEA 2 _P49 (SEQ ID NO. 52), or HUMA1ACM_PEA 2 _P59 (SEQ
CC ID NO. 53); an isolated polypeptide encoding for a head of: (a)
CC HUMA1ACM_PEA 2 _P36 comprising a polypeptide 70% homologous to SEQ ID NO.
CC 180 or 182 of HUMA1ACM_PEA 2 _P36; (b) HUMA1ACM_PEA 2 _P49 comprising a
CC polypeptide 70% homologous to SEQ ID NO. 182 of HUMA1ACM_PEA 2 _P49; or
CC (c) HUMA1ACM_PEA 2 _P59 comprising a polypeptide 70% homologous to SEQ ID
CC NO. 182 of HUMA1ACM_PEA 2 _P59; an isolated polypeptide encoding for a
CC tail of: (a) HUMA1ACM_PEA 2 _P36 comprising a polypeptide 70% homologous
CC to SEQ ID NO. 181 in HUMA1ACM_PEA 2 _P36; (b) HUMA1ACM_PEA 2 _P49
CC comprising a polypeptide 70% homologous to SEQ ID NO. 183 in HUMA1ACM_PEA
CC 2 _P49; or (c) HUMA1ACM_PEA 2 _P59 comprising a polypeptide 70%


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Query Match      100.0%;   Score 350;   DB 2;   Length 699;
Best Local Similarity 100.0%;
Matches    58;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
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Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 ||||||||||||||||||
 Db 483 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

Search completed: November 23, 2009, 11:14:49
Job time : 58 secs

SCORE 3.0